

<110> Merck & Co., Inc.

<130> 21471 PCT

<151> 2004-01-09

<170> FastSEQ for Windows Version 4.0

<211> 571

<213> Artificial Sequence

<223> modified HCV NS5B

1/16

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Tyr Arg Ala Cys Ser Leu Pro Glu Glu Ala His Thr Ala Ile His Ser
                245                250                255
Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly
                260                265                270
Gln Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
                275                280                285
Ser Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys
                290                295                300
Lys Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp
305                310                315                320
Leu Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn
                325                330                335
Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
                340                345                350
Asp Pro Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
                355                360                365
Ser Asn Val Ser Val Ala Leu Gly Pro Gln Gly Arg Arg Arg Tyr Tyr
370                375                380
Leu Thr Arg Asp Pro Thr Thr Pro Ile Ala Arg Ala Ala Trp Glu Thr
385                390                395                400
Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
                405                410                415
Ala Pro Thr Ile Trp Ala Arg Met Val Leu Met Thr His Phe Phe Ser
                420                425                430
Ile Leu Met Ala Gln Asp Thr Leu Asp Gln Asn Leu Asn Phe Glu Met
                435                440                445
Tyr Gly Ala Val Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
450                455                460
Glu Arg Leu His Gly Leu Asp Ala Phe Ser Leu His Thr Tyr Thr Pro
465                470                475                480
His Glu Leu Thr Arg Val Ala Ser Ala Leu Arg Lys Leu Gly Ala Pro
                485                490                495
Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
500                505                510
Ile Ser Arg Gly Gly Arg Ala Ala Val Cys Gly Arg Tyr Leu Phe Asn
515                520                525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Arg
530                535                540
Leu Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
545                550                555                560
Ile Tyr His Ser Val Ser Arg Ala Arg Pro Arg
                565                570

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<210> 2

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 2

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Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly
1                5                10                15

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Pro	Glu	Glu	Glu	Lys	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Asn	Ser	Leu	Met	20	25	30
Arg	Phe	His	Asn	Lys	Val	Tyr	Ser	Thr	Thr	Ser	Arg	Ser	Ala	Ser	Leu	35	40	45
Arg	Ala	Lys	Lys	Val	Thr	Phe	Asp	Arg	Val	Gln	Val	Leu	Asp	Ala	His	50	55	60
Tyr	Asp	Ser	Val	Leu	Gln	Asp	Val	Lys	Arg	Ala	Ala	Ser	Lys	Val	Ser	65	70	75
Ala	Arg	Leu	Leu	Thr	Val	Glu	Glu	Ala	Cys	Ala	Leu	Thr	Pro	Pro	His	85	90	95
Ser	Ala	Lys	Ser	Arg	Tyr	Gly	Phe	Gly	Ala	Lys	Glu	Val	Arg	Ser	Leu	100	105	110
Ser	Arg	Arg	Ala	Val	Asn	His	Ile	Arg	Ser	Val	Trp	Glu	Asp	Leu	Leu	115	120	125
Glu	Asp	Gln	His	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	130	135	140
Val	Phe	Cys	Ile	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Pro	Ala	Arg	Leu	145	150	155
Ile	Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	165	170	175
Tyr	Asp	Ile	Ala	Gln	Lys	Leu	Pro	Lys	Ala	Ile	Met	Gly	Pro	Ser	Tyr	180	185	190
Gly	Phe	Gln	Tyr	Ser	Pro	Ala	Glu	Arg	Val	Asp	Phe	Leu	Leu	Lys	Ala	195	200	205
Trp	Gly	Ser	Lys	Lys	Asp	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	210	215	220
Phe	Asp	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	225	230	235
Tyr	Gln	Ala	Cys	Ser	Leu	Pro	Gln	Glu	Ala	Arg	Thr	Val	Ile	His	Ser	245	250	255
Leu	Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Thr	Asn	Ser	Lys	Gly	260	265	270
Gln	Ser	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	275	280	285
Ser	Met	Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Leu	Ala	Ala	Cys	290	295	300
Lys	Ala	Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	305	310	315
Leu	Val	Val	Ile	Ser	Glu	Ser	Gln	Gly	Asn	Glu	Glu	Asp	Glu	Arg	Asn	325	330	335
Leu	Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	340	345	350
Asp	Leu	Pro	Arg	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	355	360	365
Ser	Asn	Val	Ser	Val	Ala	Leu	Asp	Ser	Arg	Gly	Arg	Arg	Arg	Tyr	Phe	370	375	380
Leu	Thr	Arg	Asp	Pro	Thr	Thr	Pro	Ile	Thr	Arg	Ala	Ala	Trp	Glu	Thr	385	390	395
Val	Arg	His	Ser	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Gln	Tyr	405	410	415
Ala	Pro	Thr	Ile	Trp	Val	Arg	Met	Val	Ile	Met	Thr	His	Phe	Phe	Ser	420	425	430
Ile	Leu	Leu	Ala	Gln	Asp	Thr	Leu	Asn	Gln	Asn	Leu	Asn	Phe	Glu	Met	435	440	445

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Tyr Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile
  450          455          460
Glu Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro
465          470          475          480
His Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro
          485          490          495
Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
          500          505          510
Ile Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn
          515          520          525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser
          530          535          540
Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
545          550          555          560
Ile Tyr His Ser Val Ser His Ala Arg Pro Arg
          565          570

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<210> 3
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified HCV NS5B

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<400> 3
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser
  1          5          10          15
Ala Glu Glu Glu Lys Leu Pro Ile Ser Pro Leu Ser Asn Ser Leu Leu
          20          25          30
Arg His His Asn Leu Val Tyr Ser Thr Ser Ser Arg Ser Ala Ser Gln
          35          40          45
Arg Gln Arg Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
          50          55          60
Tyr Lys Thr Ala Leu Lys Glu Val Lys Glu Arg Ala Ser Arg Val Lys
65          70          75          80
Ala Arg Met Leu Thr Ile Glu Glu Ala Cys Ala Leu Val Pro Pro His
          85          90          95
Ser Ala Arg Ser Lys Phe Gly Tyr Ser Ala Lys Asp Val Arg Ser Leu
          100          105          110
Ser Ser Arg Ala Ile Asp Gln Ile Arg Ser Val Trp Glu Asp Leu Leu
          115          120          125
Glu Asp Thr Thr Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
          130          135          140
Val Phe Cys Val Asp Pro Ala Lys Gly Gly Arg Lys Pro Ala Arg Leu
145          150          155          160
Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Arg Ala Leu
          165          170          175
Tyr Asp Val Ile Gln Lys Leu Ser Ile Glu Thr Met Gly Ser Ala Tyr
          180          185          190
Gly Phe Gln Tyr Ser Pro Gln Gln Arg Val Glu Arg Leu Leu Lys Met
          195          200          205
Trp Thr Ser Lys Lys Thr Pro Leu Gly Phe Ser Tyr Asp Thr Arg Cys
210          215          220

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Phe	Asp	Ser	Thr	Val	Thr	Glu	Gln	Asp	Ile	Arg	Val	Glu	Glu	Glu	Ile
225					230					235					240
Tyr	Gln	Cys	Cys	Asn	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Ser	Ser
				245					250						255
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly
			260					265					270		
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr
		275					280					285			
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala
	290					295				300					
Lys	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp
305				310						315					320
Leu	Val	Val	Val	Ala	Glu	Ser	Asp	Gly	Val	Asp	Glu	Asp	Arg	Ala	Ala
			325					330							335
Leu	Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly
			340					345					350		
Asp	Ala	Pro	Gln	Pro	Thr	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser
		355					360					365			
Ser	Asn	Val	Ser	Val	Ala	Arg	Asp	Asp	Lys	Gly	Arg	Arg	Tyr	Tyr	Tyr
	370					375					380				
Leu	Thr	Arg	Asp	Ala	Thr	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr
385					390					395					400
Ala	Arg	His	Thr	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Met	Tyr
			405					410						415	
Ala	Pro	Thr	Ile	Trp	Val	Arg	Met	Val	Met	Met	Thr	His	Phe	Phe	Ser
			420					425					430		
Ile	Leu	Gln	Ser	Gln	Glu	Ile	Leu	Asp	Arg	Pro	Leu	Asp	Phe	Glu	Met
		435					440					445			
Tyr	Gly	Ala	Thr	Tyr	Ser	Val	Thr	Pro	Leu	Asp	Leu	Pro	Ala	Ile	Ile
	450					455					460				
Glu	Arg	Leu	His	Gly	Leu	Ser	Ala	Phe	Thr	Leu	His	Ser	Tyr	Ser	Pro
465					470					475					480
Val	Glu	Leu	Asn	Arg	Val	Ala	Gly	Thr	Leu	Arg	Lys	Leu	Gly	Cys	Pro
			485					490						495	
Pro	Leu	Arg	Ala	Trp	Arg	His	Arg	Ala	Arg	Ala	Val	Arg	Ala	Lys	Leu
			500					505					510		
Ile	Ala	Gln	Gly	Gly	Lys	Ala	Lys	Ile	Cys	Gly	Leu	Tyr	Leu	Phe	Asn
		515					520					525			
Trp	Ala	Val	Arg	Thr	Lys	Thr	Asn	Leu	Thr	Pro	Leu	Pro	Ala	Thr	Gly
	530					535					540				
Gln	Leu	Asp	Leu	Ser	Ser	Trp	Phe	Thr	Val	Gly	Val	Gly	Gly	Asn	Asp
545					550					555					560
Ile	Tyr	His	Ser	Val	Ser	Arg	Ala	Arg	Thr	Arg					
				565					570						

<210> 4

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 4

Met	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Val	Thr	Pro	Cys	Ala
1				5					10					15	
Ala	Glu	Glu	Ser	Lys	Leu	Pro	Ile	Ser	Pro	Leu	Ser	Asn	Ser	Leu	Leu
			20					25					30		
Arg	His	His	Asn	Met	Val	Tyr	Ala	Thr	Thr	Thr	Arg	Ser	Ala	Val	Thr
			35				40					45			
Arg	Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln	Val	Val	Asp	Ser	His
			50			55					60				
Tyr	Asn	Glu	Val	Leu	Lys	Glu	Ile	Lys	Ala	Arg	Ala	Ser	Arg	Val	Lys
65					70					75					80
Ala	Arg	Leu	Leu	Thr	Thr	Glu	Glu	Ala	Cys	Asp	Leu	Thr	Pro	Pro	His
				85					90					95	
Ser	Ala	Arg	Ser	Lys	Phe	Gly	Tyr	Gly	Ala	Lys	Asp	Val	Arg	Ser	His
			100					105						110	
Ser	Arg	Lys	Ala	Ile	Asn	His	Ile	Ser	Ser	Val	Trp	Lys	Asp	Leu	Leu
			115				120					125			
Asp	Asp	Asn	Asn	Thr	Pro	Ile	Pro	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu
			130			135					140				
Val	Phe	Ala	Val	Asn	Pro	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu
145					150					155					160
Ile	Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Arg	Ala	Leu
				165					170					175	
His	Asp	Val	Ile	Lys	Lys	Leu	Pro	Glu	Ala	Val	Met	Gly	Ala	Ala	Tyr
			180					185					190		
Gly	Phe	Gln	Tyr	Ser	Pro	Ala	Gln	Arg	Val	Glu	Phe	Leu	Leu	Thr	Ala
			195				200					205			
Trp	Lys	Ser	Lys	Lys	Thr	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys
			210			215					220				
Phe	Asp	Ser	Thr	Val	Thr	Glu	Lys	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val
225					230					235					240
Tyr	Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala
				245					250					255	
Leu	Thr	Asp	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	His	Asn	Ser	Lys	Gly
				260				265					270		
Asp	Leu	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr
			275				280					285			
Ser	Phe	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Ile
			290			295					300				
Arg	Ala	Ala	Gly	Leu	Arg	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp
305					310					315					320
Leu	Val	Val	Ile	Ala	Glu	Ser	Asp	Gly	Val	Glu	Glu	Asp	Asn	Arg	Ala
				325					330					335	
Leu	Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly
			340				345						350		
Asp	Ala	Pro	Gln	Pro	Ala	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser
			355				360					365			
Ser	Asn	Val	Ser	Val	Ala	His	Asp	Val	Thr	Gly	Lys	Lys	Val	Tyr	Tyr
			370			375					380				
Leu	Thr	Arg	Asp	Pro	Glu	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr
385					390					395					400
Val	Arg	His	Thr	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Val	Tyr
				405					410					415	
Ala	Pro	Thr	Ile	Trp	Val	Arg	Met	Ile	Leu	Met	Thr	His	Phe	Phe	Ser
			420					425					430		

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Ile Leu Gln Ser Gln Glu Ala Leu Glu Lys Ala Leu Asp Phe Asp Met
    435                      440                      445
Tyr Gly Val Thr Tyr Ser Ile Thr Pro Leu Asp Leu Pro Ala Ile Ile
    450                      455                      460
Gln Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Gly Tyr Ser Pro
465                      470                      475                      480
His Glu Leu Asn Arg Val Ala Gly Ala Leu Arg Lys Leu Gly Val Pro
    485                      490                      495
Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
    500                      505                      510
Ile Ala Gln Gly Gly Arg Ala Lys Ile Cys Gly Ile Tyr Leu Phe Asn
    515                      520                      525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Ala Ala Ala
    530                      535                      540
Lys Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
545                      550                      555                      560
Ile Tyr His Ser Met Ser His Ala Arg Pro Arg
    565                      570

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<210> 5
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified HCV NS5B

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<400> 5
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
1                      5                      10                      15
Ala Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Ile
    20                      25                      30
Arg His His Asn Met Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu
    35                      40                      45
Arg Gln Lys Lys Val Thr Phe Asp Arg Val Gln Val Phe Asp Gln His
    50                      55                      60
Tyr Gln Glu Ile Leu Lys Glu Ile Lys Leu Arg Ala Ser Lys Val Gln
65                      70                      75                      80
Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Asp Leu Thr Pro Ser His
    85                      90                      95
Ser Ala Arg Ser Lys Tyr Gly Tyr Gly Ala Gln Asp Val Arg Ser His
    100                     105                     110
Ala Ser Lys Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu
    115                     120                     125
Glu Asp Ser Asp Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
    130                     135                     140
Val Phe Cys Val Asp Pro Ser Lys Gly Gly Arg Lys Pro Ala Arg Leu
145                     150                     155                     160
Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
    165                     170                     175
Tyr Asp Val Thr Gln Lys Leu Pro Gln Ala Val Met Gly Ser Ala Tyr
    180                     185                     190
Gly Phe Gln Tyr Ser Pro Thr Gln Arg Val Glu Tyr Leu Leu Lys Met
    195                     200                     205

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Trp Arg Ser Lys Lys Val Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210                215                220
Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Asn Asp Ile
225                230                235                240
Tyr Gln Ser Cys Gln Leu Asp Pro Val Ala Arg Arg Ala Val Ser Ser
                245                250                255
Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Val Asn Ser Lys Gly
                260                265                270
Gln Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
                275                280                285
Ser Met Gly Asn Thr Ile Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys
                290                295                300
Arg Ala Ala Asn Ile Lys Asp Cys Asp Met Leu Val Cys Gly Asp Asp
305                310                315                320
Leu Val Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Thr Glu Ser
                325                330                335
Leu Arg Ala Phe Thr Asp Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
                340                345                350
Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
                355                360                365
Ser Asn Val Ser Val Ala His Asp Gly Asn Gly Lys Arg Tyr Tyr Tyr
                370                375                380
Leu Thr Arg Asp Cys Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
385                390                395                400
Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe
                405                410                415
Ala Pro Thr Ile Trp Val Arg Met Val Leu Met Thr His Phe Phe Ser
                420                425                430
Ile Leu Gln Ser Gln Glu Gln Leu Glu Lys Ala Leu Asp Phe Asp Ile
                435                440                445
Tyr Gly Val Thr Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
                450                455                460
Gln Arg Leu His Gly Met Ala Ala Phe Ser Leu His Gly Tyr Ser Pro
465                470                475                480
Val Glu Leu Asn Arg Val Gly Ala Cys Leu Arg Lys Leu Gly Val Pro
                485                490                495
Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
                500                505                510
Ile Ala Gln Gly Gly Lys Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn
                515                520                525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Val Ser Ala Ser
                530                535                540
Lys Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Asp Gly Gly Asp
545                550                555                560
Ile Tyr His Ser Val Ser Gln Ala Arg Pro Arg
                565                570

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<210> 6

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 1

<400> 6

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accacaacaa agagcgctc actaagggtc aaaaaggtaa cttttgatag gatgcaagt 180
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gccaaaaatg aggtgttctg cgtggacccc accaaggggg gcaagaaagc agctcgcctt 480
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tatcgggcct gctccttgcc cgaggaggcc cacttgcca tacactcgt aactgagaga 780
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gtctcggtc gatattctct caactgggag gtgaagacca agctcaaaact cactccattg 1620
cgggaggcgc gcctcctgga tttatccagc tgggtcaccg tcggcgccgg cgggggagac 1680
atztatcaca gcgtgtcgcg tgcccgacca cgc 1713

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<210> 7

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 2

<400> 7

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acaacctcaa ggagtgcctc tctgagggca aagaagggtga cttttgacag ggtgcagggt 180
ctggacgcac actatgactc agtcttgacg gacgttaagc gggcgccctc taaggttagt 240
gcgaggctcc tcacggtaga ggaagcctgc gcgctgacct cgccccactc cgccaaatcg 300
cgatacggat ttggggcaaa agagggtgag agcttatcca ggaggggcgt taaccacatc 360
cggtcctgtg gggaggacct cctggaagac caacataccc caattgacac aactatcatg 420
gctaaaaatg aggtgttctg cattgatcca actaaagggt ggaaaaagcc agctcgcctc 480
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cgggtcgatt tcctcctcaa agcttgggga agtaagaagg acccaatggg gttctcgtat 660
gacaccgctt gctttgactc aaccgtcacg gagagggaca taagaacaga agaatccata 720
tatcaggctt gttctctgcc tcaagaagcc agaactgtca tacactcgt cactgagaga 780
ctttacgtag gagggcccat gacaaacagc aaagggcaat cctgcggcta caggcggttg 840
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cttgccagcgt gtaaggctgc agggatcgtg gaccctgtta tgttggtgtg tggagacgac 960
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gtaagacact cccctgtcaa ttcttggtg ggcaacatca tccagtagcg cccacaatc 1260
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<210> 8

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 3

<400> 8

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acgtcgtcga gaagcgcttc ccagcgtcag aggaagggtta ccttcgacag actgcagggtg 180
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gcccgcattg tcaccatgca ggaagcgtgc gcgtcgtcc ctctcactc tgcccggctc 300
aagttcgggt atagtgcgaa ggacgttcgc tccttggtcca gcagggccat tgaccagatc 360
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gcgaagaacg aggtgttttg tgtggacccc gctaaagggg gccgcaagcc cgctcgcttc 480
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cgggtcgaac gtctactgaa gatgtggacc tcaaagaaaa cccccttggg gttctcatat 660
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ccagccactg gccagttgga cttgtccagc tggtttacgg ttggtgtcgg cgggaacgac 1680
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<210> 9

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 4

<400> 9

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gtggacagtc actacaatga agtgcttaag gagataaagg cacgagcatc cagagtgaag 240
gcacgcttgc ttaccacaga ggaagcttgc gacctgacgc cccccactc agccagatca 300
aagttcggct acggggcgaa ggatgttcgg agccattccc gcaaggccat taaccacatc 360
agctccgtgt ggaaggactt gctggacgac aacaataccc caataccaac aacaatcatg 420
gccaaaaatg aggtcttcgc tgtgaaccca gcgaaggag gtcggaagcc tgctcgcctg 480
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cgggtggaat ttcttctgac tgcttggaag tcgaagaaga cccaatggg gttctcttat 660
gatacccgct gctttgactc cactgtaacc gaaaaggaca tcagggtcga ggaagaggtc 720
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cctgccgctg ccaaactcga tttatcgggt tggtttacgg taggcgccgg cgggggagac 1680
atztatcaca gcatgtctca tgcccagacc cgc

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<210> 10

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 5

<400> 10

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accacatcac gcagcgccag cctccgccag aagaagggtca catttgacag agtgcaagtg 180
ttcgaccaac attaccagga aatactaaag gagattaagc ttcgagcgtc caaggtgcag 240
gcgaagctct tatccgtaga ggaagcctgc gacctcacac catcgactc agcccgggtc 300
aaatatgggt atggtgcaca ggacgttaga agccatgcta gcaaggccgt caaccacatc 360
cgctccgtgt gggaggactt gctagaagac tctgatactc caattcccac aaccatcatg 420
gctaagaatg aagtcttctg cgtagatccg tcgaagggtg gacgcaagcc ggcacgctta 480

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atagttttacc cagacttggg cgtgcgggtc tgcgagaaga tggccctata cgacgtcacg 540
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agggttgagt acctgctcaa aatgtggcgg tcaaagaagg tgcctatggg cttttcttac 660
gacaccaggt gttttgattc aaccgtcact gagcgggaca tccggactga gaacgacatc 720
tatcagtctt gccagctgga tcccgtagca aggagggcag tatcatccct aacggaacgg 780
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gtctccgcga gcaagcttga cttatcaggc tggttcgtgg ccggctacga cgggggggac 1680
atztatcaca gcgtgtccca ggctcgacc cgt 1713

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<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 11

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24

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

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34

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

tcatactctt ggaccggggc tct

23

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
gtgccgctct atcgagcggg gagt

24

<210> 15
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 15
atactcctgg acaggggccc t

21

<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
atactcctgg acaggggccc t

21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ccgctctacc gagcgggggag t

21

<210> 18

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
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24

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
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30

<210> 20
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<220>
 <223> Primer

<400> 20
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21

<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 21
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24

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 22
 gttc gatgtc atactcgtgg actg

24

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 23
 aagctgccta ccgagcaggc agca

24

<210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 24
 ctaagctcag gctcttggtc cact

24

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 25
 gacgacgtcg tatgttggtc catg

24

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 26
 ctaccgagcg gggagcaaaa agatg

25

<210> 27
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-Tag

<400> 27
 Leu Glu His His His His His His
 1 5

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence encoding SEQ ID NO: 27

<400> 28
ctcgagcacc accaccacca ccac

24